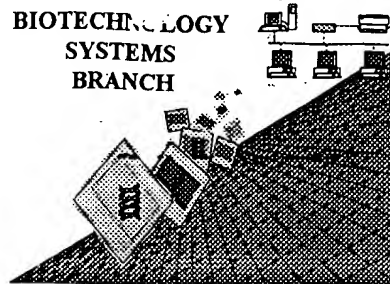


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/729,658

Source: 01/PE

Date Processed by STIC: 12/12/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/729658

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/729,658

DATE: 12/12/2000
 TIME: 11:07:55

Input Set : A:\55924.app
 Output Set: N:\CRF3\12122000\I729658.raw

Does Not Comply
 Corrected Diskette Needed

3 <119> APPLICANT: Lonana et al.
 5 <129> TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
 7 <130> FILE REFERENCE: 55924
 9 <140> CURRENT APPLICATION NUMBER: US/09/729,658
 10 <141> CURRENT FILING DATE: 2000-12-04
 12 <150> PRIOR APPLICATION NUMBER: 09/342,681
 13 <151> PRIOR FILING DATE: 1999-06-29
 15 <150> PRIOR APPLICATION NUMBER: 60/092,279
 16 <151> PRIOR FILING DATE: 1998-07-09
 18 <150> PRIOR APPLICATION NUMBER: 60/112,366
 19 <151> PRIOR FILING DATE: 1998-12-15
 21 <160> NUMBER OF SEQ ID NOS: 122
 23 <170> SOFTWARE: PatentIn Ver. 2.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 1574
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Homo sapiens
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (242)..(1417)
 34 <400> SEQUENCE: 1
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 37 cggagtagag ctacacatgc ggtctctccc tctctcgtcc cggccagcca ctctcggcca 120
 39 ggaacgggtc cctcagccc ccaagccatg ccagacacgt agccgcctgt cagaggtcgt 180
 41 gaacggctga qccagacgca ccggtctccc ggcctcagga gattgggtat ctccggaggg 240
 43 c atg ggc tac ccg gag gtg gag cgc agc gaa ctc ctg cct gca gca gca 289
 44 Met Gly Tyr Pro Glu Val Glu Arg Arg Glu Leu Leu Pro Ala Ala Ala
 45 1 5 10 15
 17 ccg cgg gag cga ggg agc caa ggc tgc ggg tgt ggc ggg gcc cct gcc 337
 48 Pro Arg Glu Arg Gly Ser Glu Gly Cys Gly Cys Gly Gly Ala Pro Ala
 49 20 25 30
 51 cgg ggc ggc gaa ggg aac agc tgc ctg ctc ttc ctg ggt ttc ttt ggc 385
 52 Arg Ala Gly Glu Gly Asn Ser Cys Leu Leu Phe Leu Gly Phe Phe Gly
 53 35 40 45
 55 ctc tcg ctg gcc ctc caa ctg ctg acg ttg tgc tgc tac cta gag ttg 433
 56 Leu Ser Leu Ala Leu His Leu Leu Thr Leu Cys Cys Tyr Leu Glu Leu
 57 50 55 60
 59 cgc tcg gag ttg cgg cgg gaa cgt gga gcc gaa tcc cgc ctt ggc ggc 481
 60 Arg Ser Glu Leu Arg Arg Glu Arg Gly Ala Glu Ser Arg Leu Gly Gly
 61 65 70 75 80
 63 tcg gcc acc cct ggc acc tct ggc acc cta agc agc ctc ggt ggc ctc 529
 64 Ser Gly Thr Pro Gly Thr Ser Gly Thr Leu Ser Ser Leu Gly Gly Leu
 65 85 90 95
 67 gac cct gac agc ccc atc acc agt cac ctt gag cag ccg tca cct aug 577
 68 Asp Pro Asp Ser Pro Ile Thr Ser His Leu Gly Glu Pro Ser Pro Lys
 69 100 105 110
 71 cag cag cca ttg gaa ccg gga gaa gcc gca ctc cac tct gac tcc cag 625

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/729,658

DATE: 12/12/2000

TIME: 12:07:55

Input Set : A:\55924.app

Output Set: N:\CRF3\12122000\I729658.raw

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72 Gln Gln Pro Leu Glu Pro Gly Glu Ala Ala Leu His Ser Asp Ser Gln
73      115      120      125
75 gac ggg cac caq atg gcc cta ttg aat ttc ttc ttc cct gat gaa aag 673
76 Asp Glu His Gln Met Ala Leu Leu Asn Phe Phe Phe Pro Asp Glu Lys
77      130      135      140
79 cca tac tct gaa gaa gaa agt agg cct att cgc cgc aat aaa aga aac 721
80 Pro Tyr Ser Glu Glu Glu Ser Arg Arg Val Arg Arg Asn Lys Arg Ser
81 145      150      155      160
83 aaa agc aat gaa gga gaa gat gcc cca gtt aaa aac aag aaa aag gga 769
84 Lys Ser Asn Glu Gly Ala Asp Gly Pro Val Lys Asn Lys Lys Lys Gly
85      165      170      175
87 aag aaa gca gga cct cct gga ccc aat gcc cct cca gga ccc cca gga 817
88 Lys Lys Ala Gly Pro Pro Gly Pro Asn Gly Pro Pro Gly Pro Pro Gly
89      180      185      190
91 cct cca gga ccc caq gga ccc cca gga att cca gga att cct gga att 865
92 Pro Pro Gly Pro Gln Gly Pro Pro Gly Ile Pro Gly Ile Pro Gly Ile
93      195      200      205
95 cca gga aca act att atg gga cca cct ggt cct cca ggt cct cct ggt 913
96 Pro Gly Thr Thr Val Met Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly
97      210      215      220
99 cct cca gga ccc cct gcc ctc caq gga cct tct ggt gct gct gat aaa 961
100 Pro Gln Gly Pro Pro Gly Leu Gln Gly Pro Ser Gly Ala Ala Asp Lys
101 225      230      235      240
103 gct gga act cga gaa aac caq cca gct gtg gta cat cta caq gcc caa 1009
104 Ala Gly Thr Arg Glu Asn Gln Pro Ala Val Val His Leu Gln Gly Gln
105      245      250      255
107 gag tca cca att cca gtc aag aat gat ctt tca ggt gga gta ctc aat 1057
108 Gly Ser Ala Ile Gln Val Lys Asn Asp Leu Ser Gly Gly Val Leu Asn
109      260      265      270
111 gac tgg tct cgc atc act atg aac ccc aag gtg ttt aag cta cat ccc 1105
112 Asp Trp Ser Arg Ile Thr Met Asn Pro Lys Val Phe Lys Leu His Pro
113      275      280      285
115 cgc agc ggg gag ctg gag gta ctg gtg gac gcc acc tac ttc atc tat 1153
116 Arg Ser Gly Glu Leu Glu Val Leu Val Asp Gly Thr Tyr Phe Ile Tyr
117      290      295      300
119 aqt caq gta gaa gta tac tac atc aac ttc act gac ttt gcc agc tat 1201
120 Ser Gln Val Glu Val Tyr Tyr Ile Asn Phe Thr Asp Phe Ala Ser Tyr
121 305      310      315      320
123 gag atg gta gta gta gat gag aag ccc ttc ctg cag tgc aca cgc agc atc 1249
124 Glu Val Val Val Asp Glu Lys Pro Phe Leu Gln Cys Thr Arg Ser Ile
125      325      330      335
127 gag acg gcc aag acc aac tac aac act tgc tat acc gca gcc gtc tgc 1297
128 Glu Thr Gly Lys Thr Asn Tyr Asn Thr Cys Tyr Thr Ala Gly Val Cys
129      340      345      350
131 ctc ctc aag gcc cgg cag aag atc gcc gtc aag atg gta cac gct gac 1345
132 Leu Leu Lys Ala Arg Gln Lys Ile Ala Val Lys Met Val His Ala Asp
133      355      360      365
135 atc tcc atc aac atg agc aag cac acc acg ttc ttt ggg gcc atc aag 1393
136 Ile Ser Ile Asn Met Ser Lys His Thr Thr Phe Phe Gly Ala Ile Arg

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/729,658

DATE: 12/12/2000

TIME: 12:07:55

Input Set : A:\55924.app

Output Set: N:\CRF3\12122000\I729658.raw

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137      370      375      380
139 cta ggt gaa gcc cct gca tcc tag attcccccaat ttgacctctg tccgtgcccc 1447
140 leu gly gln ala pro ala ser
141 385      390
143 tccctgggt ttggagcca agacccccaa aacctctaaq tctctctg gactgagtg 1507
145 tattgggttt gaggcgagc agaatgcgc cattgttatt tatccccag tgaactcag 1507
147 ttgacaa 1574
150 <210> SEQ ID NO: 2
151 <211> LENGTH: 391
152 <212> TYPE: PRP
153 <213> ORGANISM: Homo sapiens
155 <400> SEQUENCE: 2
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157 1 5 10 15
158 Pro Arg Glu Arg Gly Ser Gln Gly Cys Gly Cys Gly Gly Ala Pro Ala
159 20 25 30
160 Arg Ala Gly Glu Gly Asn Ser Cys Leu Leu Phe Leu Gly Phe Phe Gly
161 35 40 45
162 Leu Ser Leu Ala Leu His Leu Leu Thr Leu Cys Cys Tyr Leu Glu Leu
163 50 55 60
164 Arg Ser Glu Leu Arg Arg Glu Arg Gly Ala Glu Ser Arg Leu Gly Gly
165 65 70 75 80
166 Ser Gly Thr Pro Gly Thr Ser Gly Thr Leu Ser Ser Leu Gly Gly Leu
167 85 90 95
168 Asp Pro Asp Ser Pro Ile Thr Ser His Leu Gly Gln Pro Ser Pro Lys
169 100 105 110
170 Gln Gln Pro Leu Glu Pro Gly Glu Ala Ala Leu His Ser Asp Ser Gln
171 115 120 125
172 Asp Gly His Gln Met Ala Leu Leu Asn Phe Phe Phe Pro Asp Glu Lys
173 130 135 140
174 Pro Tyr Ser Glu Glu Glu Ser Arg Arg Val Arg Arg Asn Lys Arg Ser
175 145 150 155 160
176 Lys Ser Asn Glu Gly Ala Asp Gly Pro Val Lys Asn Lys Lys Lys Gly
177 165 170 175
178 Lys Lys Ala Gly Pro Pro Gly Pro Asn Gly Pro Pro Gly Pro Pro Gly
179 180 185 190
180 Pro Pro Gly Pro Gln Gly Pro Pro Gly Ile Pro Gly Ile Pro Gly Ile
181 195 200 205
182 Pro Gly Thr Thr Val Met Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly
183 210 215 220
184 Pro Gln Gly Pro Pro Gly Leu Gln Gly Pro Ser Gly Ala Ala Asp Lys
185 225 230 235 240
186 Ala Gly Thr Arg Glu Asn Gln Pro Ala Val Val His Leu Gln Gly Gln
187 245 250 255
188 Gly Ser Ala Ile Glu Val Lys Asn Asp Leu Ser Gly Gly Val Leu Asn
189 260 265 270
190 Asp Trp Ser Arg Ile Thr Met Asn Pro Lys Val Phe Lys Leu His Pro
191 275 280 285
192 Arg Ser Gly Glu Leu Glu Val Leu Val Asp Gly Thr Tyr Phe Ile Tyr

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/729,658

DATE: 12/12/2000

TIME: 12:07:55

Input Set : A:\55924.app

Output Set: N:\CRF3\12122000\1729658.raw

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193      290      390      490
194 Ser Gln Val Glu Val Tyr Tyr Ile Asn Phe Thr Asp Phe Ala Ser Tyr
195 305      310      315      320
196 Glu Val Val Val Asp Glu Lys Pro Phe Leu Gln Cys Thr Arg Ser Ile
197      325      330      335
198 Glu Thr Gly Lys Thr Asn Tyr Asn Thr Cys Tyr Thr Ala Gly Val Cys
199      340      345      350
200 Leu Leu Lys Ala Arg Gln Lys Ile Ala Val Lys Met Val His Ala Asp
201      355      360      365
202 Ile Ser Ile Asn Met Ser Lys His Thr Thr Phe Phe Gly Ala Ile Arg
203      370      375      380
204 Leu Gly Gln Ala Pro Ala Ser
205 385      390
209 <210> SEQ ID NO: 3
210 <211> LENGTH: 1661
211 <212> TYPE: DNA
212 <213> ORGANISM: Mus musculus
214 <220> FEATURE:
215 <221> NAME/KEY: CDS
216 <222> LOCATION: (142)..(1275)
218 <400> SEQUENCE: 3
219 Leaggaacag gteccctgcag cccccagcag atagcaggac agtagtcgcc tgtcaagggc 60
221 cgtcaagggac tgaagcagaa qcagagggctc caggagagge agaggctccc ggcctccaga 120
223 tagtgcctgt ctcgggagge c atg ggc tac cca gag gta gag cgc agg gaa 171
224 Met Gly Tyr Pro Glu Val Glu Arg Arg Glu
225      1      5      10
227 ccc ctg cct gcc gca gcc cca aag gag cgg ggc agc cag gcc tgc gcc 219
228 Pro Leu Pro Ala Ala Ala Pro Arg Glu Arg Gly Ser Gln Gly Cys Gly
229      15      20      25
231 tat cgc gag gcc cct gct cgg gcg ggc gaa ggg aac agc tgc cgg etc 267
232 Cys Arg Gly Ala Pro Ala Arg Ala Gly Glu Gly Asn Ser Cys Arg Leu
233      30      35      40
235 ttc ctg ggt ttc ttt ggc etc tgc ctg gcc etc cac ctg ctg aag ctg 315
236 Phe Leu Gly Phe Phe Gly Leu Ser Leu Ala Leu His Leu Leu Thr Leu
237      45      50      55
239 tgc tgc tac cta gag ttg cgg tcc gaa ttg cgg cgg gaa cgg gaa acc 363
240 Cys Cys Tyr Leu Glu Leu Arg Ser Glu Leu Arg Arg Glu Arg Gly Thr
241      60      65      70
243 gag tcc cgc etc ggt gcc ccg ggt gct cct gcc acc tct gcc acc cta 411
244 Glu Ser Arg Leu Gly Gly Pro Gly Ala Pro Gly Thr Ser Gly Thr Leu
245      75      80      85      90
247 agc agc cct ggg agc etc gac ccg gtc ggt ccc atc acc cgc cac ctg 459
248 Ser Ser Pro Gly Ser Leu Asp Pro Val Gly Pro Ile Thr Arg His Leu
249      95      100      105
251 agg cag ccg tcc ttt caa cag cag cct ttg gaa ccg gga gaa gat cca 507
252 Gly Gln Pro Ser Phe Gln Gln Gln Pro Leu Glu Pro Gly Glu Asp Pro
253      110      115      120
255 etc ccc cct gag tcc cag gac cgg cac cag atg gcc etc ctg aat ttc 555
256 Leu Pro Pro Glu Ser Gln Asp Arg His Gln Met Ala Leu Leu Asn Phe

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/729,658

DATE: 12/12/2000

TIME: 12:07:55

Input Set : A:\55924.app

Output Set: N:\CRF3\12122000\1729658.raw

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257          125          130          135
259 ttc ttt cct gat gaa aag gca tat tct gaa gag gaa agt aga cgt gtt 603
260 phe phe pro asp glu lys ala pyr ser glu glu glu ser arg arg val
261          140          145          150
263 cgc cgc aat aag aga agc aaa agt ggt gaa gga gca gat agt cct gtt 651
264 arg arg asn lys arg ser lys ser gly glu gly ala asp gly pro val
265 155          160          165          170
267 aaa aac aag aaa aag gga aag aag gca ggg cca cct ggg ccc aac ggc 699
268 lys asn lys lys lys gly lys lys ala gly pro pro gly pro asn gly
269          175          180          185
271 ccc cca gga cct cca gga cct ccg gga ccc cag gga cct cca ggc att 747
272 pro pro gly pro pro gly pro pro gly pro gln gly pro pro gly ile
273          190          195          200
275 cca gga att cct ggg att cca gga aca act gtt atg gga cca cct ggc 795
276 pro gly ile pro gly ile pro gly thr thr val met gly pro pro gly
277          205          210          215
279 cca cct ggc cct cct ggt cct cca gga ccc cct ggc ctc cca gga cct 843
280 pro pro gly pro pro gly pro gln gly pro pro gly leu gln gly pro
281          220          225          230
283 tct ggt gct gct gat aca act gga act cgg gaa aat cag cca gct gtg 891
284 ser gly ala ala asp lys thr gly thr arg glu asn gln pro ala val
285 235          240          245          250
287 gtg cat ctg cug ggc caa ggg tca gca att cca gtc aaa aat gat ctt 939
288 val his leu gln gly gln gly ser ala ile gln val lys asn asp leu
289          255          260          265
291 tca ggt gga gtg ctc aat gac tgg tct cgc atc act atg aac cct aag 987
292 ser gly gly val leu asn asp trp ser arg ile thr met asn pro lys
293          270          275          280
295 gtg ttt aaa cta cat ccc cgc agc ggg gag ctg gaa gtc tac tac atc 1035
296 val phe lys leu his pro arg ser gly glu leu glu val tyr tyr ile
297          285          290          295
299 aac ttc act gac ttt gcc agc tac gaa gtg qla gtg gat gaa aag ccc 1083
300 asn phe thr asp phe ala ser tyr glu val val val asp glu lys pro
301          300          305          310
303 ttc ctg cag tgc acc cgc agc att gaa aca ggg aag acc aac tac aac 1131
304 phe leu gln cys thr arg ser ile glu thr gly lys thr asn tyr asn
305 315          320          325          330
307 act tgc tat act gca ggc glg tgc ctc ctc aag gcc aag cag aaa atc 1179
308 thr cys tyr thr ala gly val cys leu leu lys ala arg gln lys ile
309          335          340          345
311 gcc glg aag atg gtg cac gct gac atc tct atc aat atg agc aag cac 1227
312 ala val lys met val his ala asp ile ser ile asn met ser lys his
313          350          355          360
315 acc acc ttc ttc ggg gcc atc aag ctg ggc gaa gcc cct gca tcc tag 1275
316 thr thr phe phe gly ala ile arg leu gly glu ala pro ala ser
317          365          370          375
319 attctcccat tccatctctgg cccatgccccc tgcgccaggt ttgggagcca ggaactccag 1345
321 aacctctaaq tgcctctgtg tctggaatga ggtatacttg cgttgcaqcc acaaagagaa 1395
323 atgcccctatg ctatllatlc cccagtgaact ccaggatgac aaggccctalg tgacltccca 1455

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<210> 5
<211> 630
<212> DNA
<213> Homo sapiens

<400> 5
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tgtgtatgg aaagatggtt ttttatggtg gctatgactg agtgggggtca acctttgact 120
gatgtacttg taatttttac agatggccct attgaatttc ttcttccctg atgaaaagcc 180
atactctgaa gaagaaagta ggcgtgttcg ccgcaataaa agaagcaaaa gcaatgaagg 240
agcagatggt aagtctactc agttgatcct ttatcacttc tgaattatth gttagtataa 300
gtatcctttt aagaactacc ttcttggtag ggcattggtg ctacgcctg taatcctagc 360
actttgggag gccacgcgg gcagatcact tgaggtgagg aattcaaaac cagcctggcc 420
aacatggtga aaccctgtct ctactaaaaa tacaaaaaaa attagccggg cctagtccca 480
gctgcttggg agactaaggc aggagaatcg cttgaaactg ggaggtagag gttgcagtga 540
gctgagactg tgccactgca ctccagcctg ggtgacagtg cgagactcca tctcaaaaaa 600
caaaaacaaa caaaaaaaaaa cactaccttt 630

see
Jan 10
on Enon
summary
sheet

FYI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/729,658

DATE: 12/12/2000

TIME: 12:07:56

Input Set : A:\55924.app

Output Set : N:\CRF3\12122000\1729658.raw

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L:2764 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:101
L:2765 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:101
L:2766 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:101
L:2767 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:101
L:2768 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:101
L:2769 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:101
L:2770 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:101
L:2775 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:101
L:2803 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:103
L:2804 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:103
L:2836 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:105
L:2837 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:105
L:2838 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:105
L:2839 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:105
L:2840 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:105
L:2841 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:105
L:2892 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:109
L:2918 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:111
L:2924 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:111
L:2925 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:111
L:2926 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:111
L:2927 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:111
L:2928 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:111
L:2929 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:111
L:2950 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:112
L:2969 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:113
L:2993 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:115
L:2994 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:115
L:2995 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:115
L:2996 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:115
L:3020 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:116
L:3022 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:116
L:3023 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:116
L:3047 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:116
L:3056 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:116
L:3057 M:341 W:(46) "n" or "Xaa" used, for SEQ ID#:116

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/729,658

DATE: 12/12/2000
TIME: 12:07:56

Input Set : A:\55924.app
Output Set : N:\CRF3\12122000\I729658.raw

L:9 M:270 C: Current Application Number differs. Replaced Application Number
L:10 M:271 C: Current Filing Date differs. Replaced Current Filing Date
L:398 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:398 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:398 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:398 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:398 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
L:493 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:9
L:493 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9
L:493 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:493 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:493 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
L:534 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:534 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:11
L:534 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:534 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11
L:534 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11
L:722 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
L:722 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:12
L:736 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
M:340 Repeated in SeqNo:12
L:744 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
L:1930 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:43
L:1930 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:43
L:1930 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:43
L:2657 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:95
L:2657 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:95
L:2657 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:95
L:2657 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:95
L:2657 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:95
L:2658 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:95
L:2658 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:95
L:2658 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:95
L:2658 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:95
M:340 Repeated in SeqNo:95
L:2659 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:95
L:2659 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:95
L:2659 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:95
L:2659 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:95
L:2662 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:95
L:2662 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:95
L:2662 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:95
L:2662 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:95
L:2693 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:97
L:2694 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:97
L:2695 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:97
L:2761 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:101
L:2762 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:101